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 NEWS 3  AUG 09  INSPEC enhanced with 1898-1968 archive
 NEWS 4  AUG 28  ADISCTI Reloaded and Enhanced
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changes
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 NEWS 8  SEP 25  CA(SM)/CAplus(SM) display of CA Lexicon
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 NEWS 14  OCT 23  Option to turn off MARPAT highlighting
enhancements available
 NEWS 15  OCT 23  CAS Registry Number crossover limit
increased to 300,000 in          multiple databases
 NEWS 16  OCT 23  The Derwent World Patents Index suite of
databases on STN          has been enhanced and reloaded
 NEWS 17  OCT 30  CHEMLIST enhanced with new search and
display field
 NEWS 18  NOV 03  JAPIO enhanced with IPC 8 features and
functionality

 NEWS EXPRESS  JUNE 30 CURRENT WINDOWS VERSION IS
V8.01b, CURRENT          MACINTOSH VERSION IS V6.0c(ENG)
AND V6.0Jc(JP),          AND CURRENT DISCOVER FILE IS DATED
26 JUNE 2006.

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implementation of IPC 8
 NEWS X25      X.25 communication option no longer available

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=> file caplus

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TOTAL                                 ENTRY   SESSION
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=> s (circular?(10a)(array? or microarray?))/bi,ab    104885
CIRCULAR?/BI                79574 CIRCULAR?/AB
156047 ARRAY?/BI                145277 ARRAY?/AB
44665 MICROARRAY?/BI                25404 MICROARRAY?/AB
L1        779 (CIRCULAR?(10A)(ARRAY? OR
MICROARRAY?))/BI,AB

=> s phagemid?/bi,ab      1165 PHAGEMID?/BI
833 PHAGEMID?/AB
L2        1165 PHAGEMID?/BI,AB

=> s l1 and l2
L3          1 L1 AND L2

=> d l3 bib ab

L3  ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2006 ACS on STN
AN  2004:120940  CAPLUS <<LOGINID::20061108>>
DN  140:176210
TI  Use of vectors forming single-stranded sense
***circular***  DNAs as probes for  ***array***  hybridization
IN  Park, Jong-Gu; Lee, Yun-Han
PA  Welgene Pharmaceuticals, Inc., S. Korea
SO  PCT Int. Appl., 38 pp. CODEN: PIXXD2
DT  Patent
LA  English
FAN.CNT 1 PATENT NO.        KIND  DATE       APPLICATION
NO.       DATE ---------------    ----  --------  ---------------------  -
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PI  WO 2004013277       A2   20040212   WO 2003-IB4955
20030725 WO 2004013277       A3   20040603    W:  AE, AG,
AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG KR 2004011602 A 20040211 KR 2002-44411 20020727 CA 2493791 AA 20040212 CA 2003-2493791 20030725 AU 2003274587 A1 20040223 AU 2003-274587 20030725 US 2004038280 A1 20040226 US 2003-627882 20030725 EP 1543167 A2 20050622 EP 2003-758562 20030725 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK CN 1678758 A 20051005 CN 2003-820929 20030725 JP 2006503558 T2 20060202 JP 2004-525717 20030725
PRAI KR 2002-44411 A 20020727 WO 2003-IB4955 W 20030725
AB A method of generating long probes for use in microarray hybridization by propagating the cloned sequences in vectors capable of generating a circular single-stranded sense DNA is described. These probes, which may be several thousand bases, are hybridized against a cDNA population to detect differences in expression profiles between cell populations. Use of ***phagemids*** to create probes from a nonredundant library on silanized slides is demonstrated. By hybridization of the sense array with Cy3 or Cy5-labeled cDNA prepns. at 60 .degree.C , 29 up-regulated and 6 down-regulated genes in cancerous liver tissue were detected.

=> s l1 not 2006/py 1112423 2006/PY
L4 701 L1 NOT 2006/PY

=> s l4 not 2005/py 1362126 2005/PY
L5 640 L4 NOT 2005/PY

=> s l5 not 2004/py 1321994 2004/PY
L6 569 L5 NOT 2004/PY

=> s l6 and (dna#1 or cdna# or (nucleic(w)acid#))/bi,ab
'#' TRUNCATION SYMBOL NOT VALID WITHIN 'DNA#1'
The truncation symbol # may be used only at the end of a search term.
To specify a variable character within a word use '!', e.g., 'wom!n' to search for both 'woman' and 'women'. Enter "HELP TRUNCATION" at an
arrow prompt (=>) for more information.

=> s l6 and (dna# or cdna# or (nucleic(w)acid#))/bi,ab
804859 DNA#/BI 622096 DNA#/AB
204460 CDNA#/BI 159210 CDNA#/AB
189751 NUCLEIC/BI 79175 NUCLEIC/AB
4737880 ACID#/BI 3186046 ACID#/AB
188731 NUCLEIC(W)ACID#
L7 24 L6 AND (DNA# OR CDNA# OR (NUCLEIC(W)ACID#))/BI,AB

=> d his
(FILE 'HOME' ENTERED AT 09:39:09 ON 08 NOV 2006)
FILE 'CAPLUS' ENTERED AT 09:39:26 ON 08 NOV 2006
L1 779 S (CIRCULAR?(10A)(ARRAY? OR MICROARRAY?))/BI,AB
L2 1165 S PHAGEMID?/BI,AB
L3 1 S L1 AND L2
L4 701 S L1 NOT 2006/PY
L5 640 S L4 NOT 2005/PY
L6 569 S L5 NOT 2004/PY
L7 24 S L6 AND (DNA# OR CDNA# OR (NUCLEIC(W)ACID#))/BI,AB

=> d l7 1-24 bib ab

L7 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:272957 CAPLUS <<LOGINID::20061108>>
DN 139:306160
TI Anti-tumor effect of in vivo IL-2 and GM-CSF electrogene therapy in murine hepatoma model
AU Chi, Chau-Hwa; Wang, Yu-Shan; Lai, Yen-Shuae; Chi, Kwan-Hwa
CS Department of Veterinary Medicine, National Taiwan University, Taiwan
SO Anticancer Research (2003), 23(1A), 315-321 CODEN: ANTRD4; ISSN: 0250-7005
PB International Institute of Anticancer Research
DT Journal
LA English
AB The authors evaluated the effect of in vivo electrogene therapy (EGT), a newly-developed gene transfer method using electroporation on the induction of anti-cancer immunity. The in vivo EGT was carried out by direct injection of plasmid ***DNAs*** encoding mouse interleukin-2 (IL-2) and granulocyte-macrophage colony-stimulating factor (GM-CSF) in a s.c. murine hepatoma model of 1MEA.7R.1 cells. Six elec. pulses were generated in situ from a square-wave electroporator fitted with a ***circular*** , six-needle electrode ***array*** . 1MEA.7R.1 cells in vitro were modified to secrete IL-2 (1MEA.7R.1/IL-2 cells). The 1MEA.7R.1/IL-2 cells had a similar cell doubling-time as their parent cells but showed a much slower growth rate in Balb/C mice. One, or 3 rounds of single gene EGT with IL-2 gene showed a dose-responsive effect of growth retardation. Co-administration of 3 rounds of IL-2/GM-CSF double gene EGT had a stronger growth inhibition effect than 3 rounds of IL-2 single gene EGT. Three rounds of IL-2/GM-CSF EGT rendered the tumor to a growth rate of stably transfected 1MEA.7R.1/IL-2 cells. Seven rounds of IL-2/GM-CSF EGT markedly inhibited the tumor growth. Reverse transcriptase-polymerase chain reaction confirmed the expression of IL-2, GM-CSF and interferon-.gamma. within treated tumors. Systemic inhibitory effects can be demonstrated from tumor-re-challenged expts. on mice which received 3 rounds of double-gene EGT. The T cell proliferation assay revealed an increased T cell proliferation in double-gene EGT-treated mice. This expt. showed that partial systemic immunity can be provoked by IL-2/GM-CSF double-gene EGT. These findings suggest that the immuno-gene therapy protocol has the potential for future clin. applications.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:735332 CAPLUS <<LOGINID::20061108>>
DN 138:34036
TI Acetylation of histone H4 by Esa1 is required for ***DNA*** double-strand break repair

AU Bird, Alexander W.; Yu, David Y.; Pray-Grant, Marilyn G.; Qiu, Qifeng; Harmon, Kirsty E.; Megee, Paul C.; Grant, Patrick A.; Smith, M. Mitchell; Christman, Michael F.
CS Department of Microbiology, University of Virginia, Charlottesville, VA, 22908, USA
SO Nature (London, United Kingdom) (2002), 419(6905), 411-415 CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English
AB Although the acetylation of histones has a well-documented regulatory role in transcription, its role in other chromosomal functions remains largely unexplored. Here we show that distinct patterns of histone H4 acetylation are essential in two sep. pathways of double-strand break repair. A budding yeast strain with mutations in wild-type H4 acetylation sites shows defects in nonhomologous end joining repair and in a newly described pathway of replication-coupled repair. Both pathways require the ESA1 histone acetyl transferase (HAT), which is responsible for acetylating all H4 tail lysines, including ectopic lysines that restore repair capacity to a mutant H4 tail. Arp4, a protein that binds histone H4 tails and is part of the Esa1-contg. NuA4 HAT complex, is recruited specifically to ***DNA*** double-strand breaks that are generated in vivo. The purified Esa1-Arp4 HAT complex acetylates linear nucleosomal ***arrays*** with far greater efficiency than ***circular*** ***arrays*** in vitro, indicating that it preferentially acetylates nucleosomes near a break site. Together, our data show that histone tail acetylation is required directly for ***DNA*** repair and suggest that a related human HAT complex may function similarly.
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:715961 CAPLUS <<LOGINID::20061108>>
DN 137:213205
TI Device for carrying out hybridization on microarrays containing an agitation unit and sample dispenser
PA Tecan Trading Ag, Switz.
SO Ger. Gebrauchsmusterschrift, 27 pp. CODEN: GGXXFR
DT Patent
LA German
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI DE 20207612 U1 20020919 DE 2002-20207612 20020515
PRAI DE 2002-20207612 20020515
AB The invention concerns a hybridization chamber for carrying out reactions on microarrays of ***DNA*** and proteins or tissues; the chamber is placed on the top of the ***microarray*** in a way that it can be ***circularly*** moved relative to the chip in order to agitate the liq. that is brought in contact with the probes that are immobilized on the chip. There is a ring sealing between the chip and the chamber; further parts are a sample application unit, fluid inflow and outflow tubes, thermostat, etc. Agitation can also be performed using a membrane pump.

L7 ANSWER 4 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:624724 CAPLUS <<LOGINID::20061108>>
DN 137:290499
TI Brownian motion of ***DNA*** confined within a two-dimensional array
AU Nykypanchuk, Dmytro; Strey, Helmut H.; Hoagland, David A.
CS Department of Polymer Science an dEngineering, University of Massachusetts Amherst, Amherst, MA, 01003, USA
SO Science (Washington, DC, United States) (2002), 297(5583), 987-990 CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal
LA English
AB Linear ***DNA*** mols. are visualized while undergoing Brownian motion inside media patterned with mol.-sized spatial constraints. The media, prepd. by colloidal templating, trap the macromols. within a two-dimensional ***array*** of spherical cavities interconnected by ***circular*** holes. Across a broad ***DNA*** size range, diffusion does not proceed by the familiar mechanisms of reptation or sieving. Rather, because of their inherent flexibility, ***DNA*** mols. strongly localize in cavities and only sporadically "jump" through holes. Jumping closely follows Poisson statistics. By reducing ***DNA*** 's configurational freedom, the holes act as mol. wt.-dependent entropic barriers. Sterically constrained macromol. diffusion underlies many sepn. methods and assumes an important role in intracellular and extracellular transport.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 5 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:644489 CAPLUS <<LOGINID::20061108>>
DN 135:206432
TI ***DNA*** array, ***DNA*** array reader, and ***DNA*** array-manufacturing apparatus
IN Iwasaki, Yutaka; Suzuki, Yoshihiko
PA Nikon Corp., Japan
SO Jpn. Kokai Tokkyo Koho, 11 pp. CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI JP 2001238674 A2 20010904 JP 2000-53312 20000229
PRAI JP 2000-53312 20000229
AB The conventional ***DNA*** array reader is accompanied with the problem of not being able to perform the reading with a high speed while maintaining a high S/N ratio such as the one gained with a confocal microscope system. A ***DNA*** array is provided, on which multiple spots of ***DNA*** probes immobilized on the baseplate are ***arrayed*** in a concentric ***circular*** shape, or a spiral shape. A ***DNA*** array reader is provided, which scans the spots of ***DNA*** probes with a high speed upon turning the array while maintaining a high S/N ratio. Diagrams describing the app. assembly are given.

L7 ANSWER 6 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:319933 CAPLUS <<LOGINID::20061108>>
DN 134:348979
TI Protein and ***cDNA*** sequences of a novel human circular canal protein 69 and diagnostic and therapeutic uses thereof
IN Mao, Yumin; Xie, Yi
PA Shanghai Bio Road Gene Development Ltd., Peop. Rep. China
SO PCT Int. Appl., 32 pp. CODEN: PIXXD2
DT Patent
LA Chinese

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------

PI WO 2001030823 A1 20010503 WO 2000-CN375 20001027 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CN 1303865 A 20010718 CN 1999-119866 19991027
PRAI CN 1999-119866 A 19991027
AB The invention provides protein and ***cDNA*** sequences for a novel human circular canal protein 69, which is a novel member of kelch protein family. The circular canal protein 69 shares sequence homol. with Drosophila kelch protein. The invention also relates to constructs and methods to express the cloned gene for the prepn. of its protein and antibodies using E.coli cells or eukaryotic cells, and diagnostic and therapeutic uses for circular canal protein 69 related diseases.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 7 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:266132 CAPLUS <<LOGINID::20061108>>
DN 135:15553
TI SWI/SNF chromatin remodeling requires changes in ***DNA*** topology
AU Gavin, Igor; Horn, Peter J.; Peterson, Craig L.
CS Program in Molecular Medicine Department of Biochemistry and Molecular Biology, University of Massachusetts Medical School, Worcester, MA, 01605, USA
SO Molecular Cell (2001), 7(1), 97-104 CODEN: MOCEFL; ISSN: 1097-2765
PB Cell Press
DT Journal
LA English
AB YSWI/SNF complex belongs to a family of enzymes that use the energy of ATP hydrolysis to remodel chromatin structure. Here we examine the role of ***DNA*** topol. in the mechanism of ySWI/SNF remodeling. We find that the ability of ySWI/SNF to enhance accessibility of nucleosomal ***DNA*** is nearly eliminated when ***DNA*** topol. is constrained in small ***circular*** nucleosomal ***arrays*** and that this inhibition can be alleviated by topoisomerases. Furthermore, we demonstrate that remodeling of these substrates does not require dramatic histone octamer movements or displacement. Our results suggest a model in which ySWI/SNF remodels nucleosomes by using the energy of ATP hydrolysis to drive local changes in ***DNA*** twist.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 8 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:266131 CAPLUS <<LOGINID::20061108>>
DN 135:15552
TI RSC unravels the nucleosome
AU Lorch, Yahli; Zhang, Mincheng; Kornberg, Roger D.
CS Department of Structural Biology, Stanford School of Medicine, Stanford, CA, 94305, USA
SO Molecular Cell (2001), 7(1), 89-95 CODEN: MOCEFL; ISSN: 1097-2765
PB Cell Press
DT Journal
LA English
AB RSC and SWI/SNF chromatin-remodeling complexes were previously reported to generate a stably altered nucleosome. We now describe the formation of hybrids between nucleosomes of different sizes, showing that the stably altered structure is a noncovalent dimer. A basis for dimer formation is suggested by an effect of RSC on the supercoiling of closed, ***circular*** ***arrays*** of nucleosomes. The effect may be explained by the interaction of RSC with ***DNA*** at the ends of the nucleosome, which could lead to the release 60-80 bp or more from the ends. ***DNA*** released in this way may be trapped in the stable dimer or lead to alternative fates such as histone octamer transfer to another ***DNA*** or sliding along the same ***DNA*** mol.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 9 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:88435 CAPLUS <<LOGINID::20061108>>
DN 135:177087
TI Stability of a human SWI-SNF remodeled nucleosomal array
AU Guyon, Jeffrey R.; Narlikar, Geeta J.; Sullivan, E. Kelly; Kingston, Robert E.
CS Department of Molecular Biology, Massachusetts General Hospital, Boston, MA, 02114, USA
SO Molecular and Cellular Biology (2001), 21(4), 1132-1144 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB SWI-SNF alters ***DNA*** -histone interactions within a nucleosome in an ATP-dependent manner. These alterations cause changes in the topol. of a closed ***circular*** nucleosomal ***array*** that persist after removal of ATP from the reaction. We demonstrate here that a remodeled closed ***circular*** ***array*** will revert toward its original topol. when ATP is removed, indicating that the remodeled array has a higher energy than that of the starting state. However, reversion occurs with a half-life measured in hours, implying a high energy barrier between the remodeled and std. states. The addn. of competitor ***DNA*** accelerates reversion of the remodeled array by more than 10-fold, and we interpret this result to mean that binding of human SWI-SNF (hSWI-SNF), even in the absence of ATP hydrolysis, stabilizes the remodeled state. In addn., we also show that SWI-SNF is able to remodel a closed ***circular*** ***array*** in the absence of topoisomerase I, demonstrating that hSWI-SNF can induce topol. changes even when conditions are highly energetically unfavorable. We conclude that the remodeled state is less stable than the std. state but that the remodeled state is kinetically trapped by the high activation energy barrier sepg. it from the unremodeled conformation.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 10 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:494777 CAPLUS <<LOGINID::20061108>>
DN 133:359597
TI Mammalian artificial chromosome formation from circular alphoid input ***DNA*** does not require telomere repeats

AU Ebersole, Thomas A.; Ross, Andrew; Clark, Elma; McGill, Niolette; Schindelhauer, Dirk; Cooke, Howard; Grimes, Brenda
CS MRC Human Genetics Unit, Western General Hospital, Edinburgh, EH4 2XU, UK
SO Human Molecular Genetics (2000), 9(11), 1623-1631 CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB Mammalian artificial chromosomes (MACs) form in HT1080 cells after transfecting linear yeast artificial chromosome constructs minimally contg. competent alphoid arrays, a selectable marker and terminal human telomere repeats. Restrictions on the structure of input ***DNA*** in MAC formation were investigated by transfecting ***circular*** or linear alphoid constructs with or without human telomere ***arrays*** and by varying the position and orientation of the telomere arrays on input linear constructs. Circular input ***DNA*** efficiently produced MACs. Absence of telomere ***arrays*** from ***circular*** input mols. did not significantly alter MAC formation rates. Linear constructs capped with telomere arrays generated MACs effectively, but a severe redn. in MAC formation was obsd. from linear constructs lacking telomere arrays. Human telomere arrays positioned 1-5 kb from linear construct ends and in either orientation were able to promote MAC formation with similar efficiencies. Both circular and linear input constructs generated artificial chromosomes that efficiently segregated in the absence of selection. Telomeres were not detected on the MACs, regardless of the inclusion of telomere ***arrays*** on input ***DNA*** , suggesting that ***circular*** chromosomes were formed. We found no evidence for acquisition of host cell ***DNA*** , which is consistent with de novo chromosome assembly.
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 11 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:305685 CAPLUS <<LOGINID::20061108>>
DN 133:256642
TI Gene delivery with optimized electroporation parameters shows potential for treatment of gliomas
AU Yoshizato, Kimio; Nishi, Toru; Goto, Tomoaki; Dev, Sukhendu B.; Takeshima, Hideo; Kino, Takeshi; Tada, Kenji; Kimura, Takahiro; Shiraishi, Shoji; Kochi, Masato; Kuratsu, Jun-Ichi; Hofmann, Gunter A.; Ushio, Yukitaka
CS Department of Neurosurgery, Kumamoto University School of Medicine, Kumamoto, 860-8556, Japan
SO International Journal of Oncology (2000), 16(5), 899-905 CODEN: IJONES; ISSN: 1019-6439
PB International Journal of Oncology
DT Journal
LA English
AB Electroporation, a std. lab. method of introducing exogenous mols. into cells, has been gaining importance as a very effective non-viral phys. technique of gene delivery. In this study, we have used s.c. model of the C6 rat glioma cells and established an optimal condition to obtain very high gene expression in tumor tissues using both reporter and functional genes. Tumors grown on the flanks of Wistar rats are exposed and directly injected with plasmid ***DNA*** having the constructs of luciferase, green fluorescent protein and, the 'A' fragment of the diphtheria toxin, DT-A. The tumors are then subjected to square wave pulses from an electroporator. Gene expression is found to be several orders of magnitude higher when the tumors are pulsed with the optimized elec. parameters compared to the controls. For luciferase, the enhancement is .apprx.135-fold, for the green fluorescent protein, gene expression is seen over a wide area within the sections examd., as contrast to a few punctate dots in the control specimens, and finally, DT-A shows massive death in the tumor tissue. A special ***circular*** ***array*** of six needles through which pulses are delivered with rotating elec. field is found to be highly efficient in transferring genes inside the tumor. Direct injection of plasmid ***DNA*** followed by electroporation allows very high in vivo gene transfer and its subsequent expression into tumor tissues. This method may be applicable to any solid tumor.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:549456 CAPLUS <<LOGINID::20061108>>
DN 131:154464
TI A capillary electrophoresis apparatus for use in ***nucleic*** ***acid*** sequencing
IN Merenkova, Irena N.; Brevnov, Maxim
PA Tetragen, S.A., Russia
SO PCT Int. Appl., 47 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 9942819 A1 19990826 WO 1999-IB465 19990219 W: AU, CA, CN, JP, RU RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE US 6103083 A 20000815 US 1998-27426 19980220 CA 2320112 AA 19990826 CA 1999-2320112 19990219 AU 9932692 A1 19990906 AU 1999-32692 19990219 AU 751105 B2 20020808 EP 1058841 A1 20001213 EP 1999-934340 19990219 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI JP 2002504681 T2 20020212 JP 2000-532710 19990219 RU 2217737 C2 20031127 RU 2000-123565 19990219
PRAI US 1998-27426 A 19980220 WO 1999-IB465 W 19990219
AB A capillary electrophoresis app. with a large no. of capillaries arranged in a curved, esp. ***circular*** , ***array*** that may be used in ***DNA*** sequencing is described. The app. requires little supervision and can be used in high throughput sequencing projects. The present invention also relates to methods of using the electrophoresis app. and methods of making the electrophoresis app.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1999:529954 CAPLUS <<LOGINID::20061108>>
DN 131:295992
TI Structural analysis of adeno-associated virus transduction circular intermediates
AU Duan, Dongsheng; Yan, Ziying; Yue, Yongping; Engelhardt, John F.
CS Department of Anatomy and Cell Biology and Department of Internal Medicine, The University of Iowa, Iowa City, IA, 52242, USA
SO Virology (1999), 261(1), 8-14 CODEN: VIRLAX; ISSN: 0042-6822
PB Academic Press

DT Journal
LA English
AB Recombinant adeno-assocd. virus (rAAV) has recently been demonstrated to form circular intermediates following transduction in muscle tissue and cell lines. Although restriction enzyme and Southern blot anal. has revealed a consistent monomer and multimer head-to-tail conformation, detailed structural sequence anal. has been lacking due to the high secondary structure of the ITR arrays. To gain further insight into potential mechanisms by which AAV circular genomes are formed from linear single-stranded viral ***DNA*** , we have performed chem. sequencing of ITR ***arrays*** within seven ***circular*** intermediates independently isolated from primary fibroblasts and Hela cells. Results from these studies demonstrated several types of circular intermediates with mosaic ITR elements flanked by two D sequences. The most predominant form consisted of a structure similar to that of previously generated AAV double-D plasmids, with one complete ITR flanked by two D-region elements. However, intermediately deleted ITR arrays with more than one complete ITR were also seen. Based on this structural information, we have proposed a model for formation of AAV circular intermediates by recombination/ligation between ITR ends of panhandle single-stranded AAV genomes. (c) 1999 Academic Press.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1997:751308 CAPLUS <<LOGINID::20061108>>
DN 128:71592
TI The yeast silent information regulator Sir4p anchors and partitions plasmids
AU Ansari, Athar; Gartenberg, Marc R.
CS Department of Pharmacology, University of Medicine and Dentistry of New Jersey-Robert Wood Johnson Medical School, Piscataway, NJ, 08854, USA
SO Molecular and Cellular Biology.(1997), 17(12), 7061-7068
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB ***Circular*** plasmids contg. telomeric TG1-3 ***arrays*** or the HMR E silencer segregate efficiently between dividing cells of the yeast Saccharomyces cerevisiae. Subtelomeric X repeats augment the TG1-3 partitioning activity by a process that requires the SIR2, SIR3, and SIR4 genes, which are also required for silencer-based partitioning. Here we show that targeting Sir4p to ***DNA*** directly via fusion to the bacterial repressor LexA confers efficient mitotic segregation to otherwise unstable plasmids. The Sir4p partitioning activity resides within a 300-amino-acid region (residues 950 to 1262) which precedes the coiled-coil dimerization motif at the extreme carboxy end of the protein. Using a topol.-based assay, we demonstrate that the partitioning domain also retards the axial rotation of LexA operators in vivo. The anchoring and partitioning properties of LexA-Sir4p chimeras persist despite the loss of the endogenous SIR genes, indicating that these functions are intrinsic to Sir4p and not to a complex of Sir factors. In contrast, inactivation of the Sir4p-interacting protein Rap1p reduces partitioning by a LexA-Sir4p fusion. The data are consistent with a model in which the partitioning and anchoring domain of Sir4p (PAD4 domain) attaches to a nuclear component that divides sym. between cells at mitosis; ***DNA*** linked to Sir4p by LexA serves as a reporter of protein movement in these expts. We infer that the segregation behavior of telomere- and silencer-based plasmids is, in part, a consequence of these Sir4p-mediated interactions. The assays presented herein illustrate two novel approaches to monitor the intracellular dynamics of nuclear proteins.
RE.CNT 71 THERE ARE 71 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:696723 CAPLUS <<LOGINID::20061108>>
DN 123:164741
TI Protein phosphatase 2A, a potential regulator of actin dynamics and actin-based organelle motility in the green alga Acetabularia
AU Menzel, Diedrik; Vugrek, Oliver; Frank, Stefan; Elsner-Menzel, Christine
CS Max-Planck-Institut fur Zellbiologie, Ladenburg, D-68526, Germany
SO European Journal of Cell Biology (1995), 67(2), 179-87
CODEN: EJCBDN; ISSN: 0171-9335
PB Wissenschaftliche Verlagsgesellschaft
DT Journal
LA English
AB The giant, unicellular alga Acetabularia is a well known exptl. model for the study of actin-dependent intracellular organelle motility. In the cyst stage, however, which is equiv. to the gametophytic stage, organelles are immobile, even though an actin cytoskeleton is present. The reason for the lack of organelle motility at this stage has not been known. To test the hypothesis that organelle motility could be under the control of posttranslational modification by protein phosphorylation, we have treated cysts with submicromolar concns. of okadaic acid or calyculin A, both potent inhibitors of serine/threonine protein phosphatases (ser/thr-PPases). The effects were dramatic: instead of linear actin bundles typical for control cysts, ***circular*** ***arrays*** of actin bundles formed in the cortical cyst cytoplasm. Concomitant with the formation of these actin rings, the cytoplasmic layers beneath the rings began to slowly rotate in a continuous and uniform counter-clockwise fashion. This effect suggests that protein phosphorylation acts on the actin cytoskeleton at two levels: (1) it changes the assembly properties of the actin filament system to the extent that novel cytoskeletal configurations are formed and (2) it raises the activity of putative motor proteins involved in the rotational movements to levels sufficiently high to support motility at a stage when organelle motility does not normally occur. Northern blot anal. of cyst stage-mRNA using probes specific to protein phosphatase type 1 (PP1) and type 2A (PP2A) reveals that PP2A is strongly expressed at this developmental stage whereas PP1 is not detectable, suggesting that PP2A is the likely target to the protein phosphatase inhibitors. As a first step in analyzing these regulatory proteins on the mol. level, we describe the complete sequence of a cyst-specific PP2A ***cDNA*** clone.

L7 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:578192 CAPLUS <<LOGINID::20061108>>
DN 123:27138
TI Replication of an rRNA gene origin plasmid in the Tetrahymena thermophila macronucleus is prevented by transcription through the origin from an RNA polymerase I promoter
AU Pan, Wei-Jun; Gallagher, Renata C.; Blackburn, Elizabeth H.
CS Dep. Microbiol. and Immunology, Univ. Calif., San Francisco, San Francisco, CA, 94143-0414, USA
SO Molecular and Cellular Biology (1995), 15(6), 3372-81
CODEN: MCEBD4; ISSN: 0270-7306

PB American Society for Microbiology
DT Journal
LA English
AB In the somatic macronucleus of the ciliate Tetrahymena thermophila, the palindromic rRNA gene (rDNA) minichromosome is replicated from an origin near the cent. of the mol. in the 5' nontranscribed spacer. The replication of this rDNA minichromosome is under both cell cycle and copy no. control. We addressed the effect on origin function of transcription through this origin region. A construct contg. a pair of 1.9-kb tandem direct repeats of the rDNA origin region, contg. the origin plus a mutated (+G), but not a wild type, rRNA promoter, is initially maintained in macronuclei as an episome. Later, linear and ***circular*** replicons with long ***arrays*** of tandem repeats accumulate (W.-J. Pan and E. H. Blackburn, ***Nucleic*** ***Acids*** Res, in press). We present direct evidence that the +G mutation inactivates this rRNA promoter. It lacks the footprint seen on the wild-type promoter and produces no detectable in vivo transcript. Independent evidence that the failure to maintain wild-type 1.9-kb repeats was caused by transcription through the origin came from placing a short ***DNA*** segment contg. the rRNA gene transcriptional termination region immediately downstream of the wild-type rRNA promoter. Insertion of this terminator sequence in the correct, but not the inverted, orientation restored plasmid maintenance. Hence, origin function was restored by inactivating the rRNA promoter through the +G mutation or causing termination before transcripts from a wild-type promoter reached the origin region. We propose that transcription by RNA polymerase I through the rDNA origin inhibits replication by preventing replication factors from assembling at the origin.

L7 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:349331 CAPLUS <<LOGINID::20061108>>
DN 122:128022
TI Computer simulation of the directional displacement of rod-shaped, arc-shaped, and ***circular*** objects in an ***array*** of obstacles, representing a simple model for the gel electrophoresis of small ***DNA***
AU Wheeler, David L.; Chrambach, Andreas
CS Sect. Macromol. Anal. Lab. Theor. Phys. Biol., Natl. Inst. Child Health Hum Dev. Natl. Inst. Health, Bethesda, MD, 20892-0001, USA
SO Biopolymers (1995), 35(2), 179-85 CODEN: BIPMAA; ISSN: 0006-3525
PB Wiley
DT Journal
LA English
AB The gel electrophoresis of ***DNA*** of identical length but various static conformations was simulated using a two-dimensional model of the movement of rod-shaped, arc-shaped, and ***circular*** objects through random ***arrays*** of disk-shaped obstacles. At low obstacle d., the displacement rate of these objects decreases from the rod-shaped to the circular approaches zero. The alignment of the arc-shaped objects along the axis of the directional movement of the objects was less than that achieved by the rod-shaped objects. Rod-shaped and arc-shaped objects were retarded in their movement by collisions with the obstacles; the no. of collisions of the former, in view of their greater ability to align, was less than that of the latter. Circular objects were exclusively retarded by collisions, while the arc-shaped objects exhibited an additional retarding mechanism, viz. the suspension ("hanging") on the obstacles. When the rigid objects were made flexible, their displacement increased. The increase was most pronounced with the circular objects, allowing them to penetrate at obstacle densities from which the rigid objects were excluded.

L7 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1995:311260 CAPLUS <<LOGINID::20061108>>
DN 122:76335
TI Matching electrostatic charge between ***DNA*** and coat protein in filamentous bacteriophage. Fiber diffraction of charge-deletion mutants
AU Symmons, Martyn F.; Welsh, Liam C.; Nave, Colin; Marvin, Don A.; Perham, Richard N.
CS Cambridge Centre Molecular Recognition, Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK
SO Journal of Molecular Biology (1995), 245(2), 86-91 CODEN: JMOBAK; ISSN: 0022-2836
PB Academic
DT Journal
LA English
AB The virion of the Ff (fd, f1, M13) filamentous bacteriophage consists of a long tube of coat protein subunits in a shingled, helical ***array*** , surrounding a genome of ***circular*** single-stranded ***DNA*** . Modified fd virions have been generated by a mutation (K48A) that removes one pos. charge from each coat protein subunit in the C-terminal region of the polypeptide chain facing the ***DNA*** . The no. of nucleotides in the mutant ***DNA*** is unchanged, but the K48A virions are 35% longer than the wild type. The authors measured the X-ray diffraction attributable to single virions in hydrated gels of wild-type and K48A bacteriophages. Most of the diffraction pattern shows no significant difference between wild-type and K48A. Since the ***DNA*** is only about 12% different by wt. of the wild-type virion, the diffraction pattern is dominated by the protein contribution, and the absence of significant differences indicates that there are no significant changes in the symmetry or structure of the protein coat. But there is a change in the diffraction pattern in a region where the ***DNA*** and protein contributions are comparable. The diffraction pattern of the K48A mutant shows an increase in intensity of one of the weaker equatorial peaks, relative to the wild type, in a region where the protein contribution has a neg. sign but the ***DNA*** contribution has a pos. sign. This is consistent with a decrease in the ratio of ***DNA*** :protein per unit length of the K48A mutant. The results suggest that the protein forms a sheath lined with pos. charges interacting electrostatically and non-specifically with a neg. charged ***DNA*** core of matching charge d. The lower pos. charge d. lining the capsid in the K48A mutant means that correspondingly fewer nucleotides can be packaged per coat protein subunit, which in turn requires an elongation of the ***DNA*** inside the virion. A longer virion is thus required to package the same amt. of ***DNA*** . Within the error of measurement, the no. of pos. charges on the protein interacting with the ***DNA*** is the same in K48A as in the wild type, despite the fact that the mutant is 35% longer than the wild type.

L7 ANSWER 19 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1990:459758 CAPLUS <<LOGINID::20061108>>
DN 113:59758
TI Adduct formation identification between phenyl glycidyl ether and 2'-deoxyadenosine and thymidine by chromatography, mass spectrometry and nuclear magnetic resonance spectroscopy
AU Van den Eeckhout, E.; De Bruyn, A.; Pepermans, H.; Esmans, E. L.; Vryens, I.; Claereboudt, J.; Claeys, M.; Sinsheimer, J. E.
CS Coll. Pharm., Univ. Ghent, Ghent, B-9000, Belg.

SO Journal of Chromatography (1990), 504(1), 113-28 CODEN: JOCRAM; ISSN: 0021-9673
DT Journal
LA English
AB Thymidine and 2'-deoxyadenosine were treated with Ph glycidyl ether in order to study the formation of the corresponding 2'-deoxynucleoside adducts. Sepn. methods were elaborated using either reversed-phase HPLC with photodiode-***array*** detection, or centrifugal ***circular*** TLC. The adducts were isolated on a preparative scale and were fully characterized by UV spectroscopy, desorption chem. ionization and fast atom bombardment mass spectrometry and 270- and 360-MHz 1H NMR spectrometry. For thymidine the main adduct was characterized as N-3-(2-hydroxy-3-phenoxypropyl)thymidine. With 2'-deoxyadenosine, predominantly N-1-(2-hydroxy-3-phenoxylpropyl)-2'-deoxyadenosine was formed. With longer reaction times, the formation of a minor amt. of dialkylated 2'-deoxyadenosine was obsd. These nucleoside adducts will be used as marker compds. for studies of ***DNA*** adduct formation.

L7 ANSWER 20 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1986:511803 CAPLUS <<LOGINID::20061108>>
DN 105:111803
TI ***DNA*** -protein interactions and ***DNA*** packaging in filamentous bacteriophages
AU Rowitch, David H.; Hunter, Gary J.; Perham, Richard N.
CS Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK
SO Biochemical Society Transactions (1986), 14(6), 1168-9 CODEN: BCSTB5; ISSN: 0300-5127
DT Journal
LA English
AB The filamentous phages fd (infecting Escherichia coli) and Pf1 (infecting Pseudomonas aeruginosa) have genomes of ***circular*** , single-stranded ***DNA*** surrounded by a tubular ***array*** of .alpha.-helical coat protein subunits. The process of phage assembly is essentially the same in the 2 viruses. An obvious difference between the fd and Pf1 coat proteins is in the clustering of pos. charged side chains (lysine and arginine residues) in the C-terminal regions. The lysine at position 48 of the C-terminus of the fd coat protein was successfully mutated to arginine and glutamine, demonstrating that a pos. charge at this site is not essential for phage assembly. Genetic engineering expts. showed that the Pf1 coat protein could not be used efficiently in fd virion assembly.

L7 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1985:482492 CAPLUS <<LOGINID::20061108>>
DN 103:82492
TI Restriction endonuclease map of pTiBo542, a potential Ti plasmid vector for genetic engineering of plants
AU Hood, Elizabeth E.; Jen, George; Kayes, Lucy; Kramer, Julie; Fraley, Robert T.; Chilton, Mary Dell
CS Dep. Biol., Washington Univ., St. Louis, MO, 63130, USA
SO Bio/Technology (1984), 2(8), 702-9 CODEN: BTCHDA; ISSN: 0733-222X
DT Journal
LA English
AB A phys. map was constructed for pTiBo542, a wide-host-range tumor-inducing plasmid of Agrobacterium tumefaciens. Forty-two fragments generated by the restriction endonuclease BamHI were arranged in a ***circular*** ***array*** using electrophoretic anal. of clones contg. overlapping segments of pTiBo542. The T- ***DNA*** region (the part of the Ti plasmid transferred to the plant) was predicted by its homol. to T- ***DNAs*** from heterologous octopine and nopaline Ti plasmids. Southern hybridizations against soybean tumor ***DNA*** using clones from this region as probes confirmed this prediction.

L7 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1985:107185 CAPLUS <<LOGINID::20061108>>
DN 102:107185
TI Involvement of circular intermediates in the transfer of T-***DNA*** from Agrobacterium tumefaciens to plant cells
AU Koukolikova-Nicola, Zdena; Shillito, Raymond D.; Hohn, Barbara; Wang, Kan; Van Montagu, Marc; Zembryski, Patricia
CS Friedrich-Miescher Inst., Basel, CH-4002, Peop. Rep. China
SO Nature (London, United Kingdom) (1985), 313(5999), 191-6 CODEN: NATUAS; ISSN: 0028-0836
DT Journal
LA English
AB The transfer of T- ***DNA*** from the Ti plasmid of Agrobacterium tumefaciens to Nicotiana tabacum plant cells was examd. for the presence of T- ***DNA*** intermediates. A ***DNA*** transformation assay was used to confirm the presence of circular intermediates. The structures may originate from circularization of T- ***DNA*** during induction of its transfer. These ***circular*** structures could produce tandem T- ***DNA*** ***arrays*** or multimeric ***circular*** structures suitable for the .lambda. packaging reaction. The circular intermediate junction site occurs precisely within the 25-base-pair terminal sequence essential for T-***DNA*** transfer.

L7 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1983:103591 CAPLUS <<LOGINID::20061108>>
DN 98:103591
TI Radiation and biophysical studies on cells and viruses, September 1, 1979-August 15, 1982
CS University of Texas, Houston, TX, USA
SO Report (1982), DOE/EV/02832-232; Order No. DE83000760, 10 pp. Avail.: NTIS From: Energy Res. Abstr. 1983, 8(1), Abstr. No. 1045
DT Report
LA English
AB The objectives were to improve the understanding of the structure and organization of the chromatin of mammalian cells throughout the cell cycle, how radiation, chems., and heat damage these structures, and how cells repair the damage. Major accomplishments include evidence that chromatids contain 8 ***circular*** , duplex ***DNA*** mols. in a side-by-side ***array*** which are pleated to form loops by periodic attachments to a well-defined backbone structure. .gamma.-Ray-induced chromosomal damage was assayed as changes in the structure of dehistonized chromosomes. Bleomycin-induced damage to chromosomal loop structures was obsd., and heat treatment was shown to have affect on structural integrity.

L7 ANSWER 24 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1983:31310 CAPLUS <<LOGINID::20061108>>
DN 98:31310
TI Injection of ***DNA*** into liposomes by bacteriophage .lambda.
AU Roessner, Charles A.; Struck, Douglas K.; Ihler, Garret M.
CS Dep. Med. Biochem., Texas A and M Coll. Med., College Station, TX, 77843, USA
SO Journal of Biological Chemistry (1983), 258(1), 643-8 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English

AB Small unilamellar vesicles (75-100 nm diam.) and large liposomes (>1 .mu.m in diam.) were prepd. contg. the lamB protein, an outer membrane protein of Escherichia coli and Shigella which serves as the receptor for bacteriophage .lambda.. Bacteriophage were obsd. to bind to these liposomes and vesicles by their tails and in most cases the heads of the bound bacteriophage appeared empty or partially empty of ***DNA*** . The .lambda. ***DNA*** was usually only partially ejected from the bacteriophage head when small unilamellar liposomes were used, presumably because the vesicles are too small to contain all the ***DNA*** . The partially ejected ***DNA*** was not susceptible to DNase unless the vesicle bilayer was 1st disrupted, suggesting that ***DNA*** injection of phage ***DNA*** into the vesicle had occurred. After disruption of these vesicles on electron microscope grids, the bacteriophage are seen to have partially empty heads and a small mass of ***DNA*** assocd. with their tails. Using larger liposomes prepd. by the fusion of lamB-bearing vesicles with polyethylene glycol and n-hexyl bromide, the heads of most of the bound bacteriophage appeared to be completely empty of ***DNA*** . Disruption of these prepns. on electron microscope grids revealed ***circular*** ***arrays*** of empty-headed bacteriophage surrounding ***DNA*** which had apparently been contained within the intact liposomes. Apparently high mol. wt. ***DNA*** can be entrapped within liposomes with high efficiency by ejection from bacteriophage .lambda.. The possible use of these ***DNA*** -contg. liposomes to facilitate gene transfer in eukaryotic cells is discussed.

=> d his
(FILE 'HOME' ENTERED AT 09:39:09 ON 08 NOV 2006)
FILE 'CAPLUS' ENTERED AT 09:39:26 ON 08 NOV 2006
L1 779 S (CIRCULAR?(10A)(ARRAY? OR MICROARRAY?))/BI,AB
L2 1165 S PHAGEMID?/BI,AB
L3 1 S L1 AND L2
L4 701 S L1 NOT 2006/PY
L5 640 S L4 NOT 2005/PY
L6 569 S L5 NOT 2004/PY
L7 24 S L6 AND (DNA# OR CDNA# OR (NUCLEIC(W)ACID#))/BI,AB

=> log y
COST IN U.S. DOLLARS SINCE FILE
TOTAL ENTRY SESSION
FULL ESTIMATED COST 116.13 116.34

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) SINCE FILE TOTAL ENTRY SESSION
CA SUBSCRIBER PRICE -18.75 -18.75

STN INTERNATIONAL LOGOFF AT 09:53:25 ON 08 NOV 2006

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Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	21844	circular near10 (array or microarray)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:19
L2	37925	435/6[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:19
L3	280	l1 and l2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:20
L4	1214015	@rlad<"20030725"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:20
L5	183	l3 and l4	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:35
L6	2	l5 and phagemid	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2006/11/08 09:36